

What is claimed is:

1. A method for identifying a subject at risk of osteoarthritis, which comprises detecting the presence or absence of one or more polymorphic variations associated with osteoarthritis in a nucleic acid sample from a subject, wherein the one or more polymorphic variations are detected in a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A, or a substantially identical sequence thereof, or a fragment of the foregoing;

whereby the presence of the polymorphic variation is indicative of the subject being at risk of osteoarthritis.

2. The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3. The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 31118000 to 31129000 of chromosome 16 in human genomic DNA.

4. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 1 selected from the group consisting of 247, 1535, 2386, 6440, 9133, 9143, 9471, 13150, 13717, 14466, 15769, 16870, 18545, 18749, 19123, 20736, 21038, 21046, 21050, 21056, 21706, 23170, 25028, 27871, 28070, 31717, 32019, 32318, 33080, 33101, 34236, 34285, 34818, 35168, 37981, 38113, 38117, 38481, 38615, 38944, 39288, 41385, 42136, 42185, 42353, 42434, 44580, 44675, 45739, 46439, 47457, 47735, 50319, 50708, 51185, 53002, 53064, 53637, 55274, 55825, 55986, 56684, 57653, 57659, 57692, 57775, 61313, 61431, 61699, 62906, 63619, 64664, 68452, 69665, 69681, 70091, 74637, 74760, 76523, 78559, 79549, 79882, 81339, 81681, 81696, 83517, 85431, 86332, 87358, 87725, 89052, 90020, 90231, 90284, 90447, 90601, 90724, 92559, 95176, 95195 and 96822.

5. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 1 selected from the group consisting of 13150, 21046, 23170, 25028, 44580, 62906, 64664 and 83517.

6. The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 36914000 to 36931000 of chromosome 4 in human genomic DNA.

7. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 2 selected from the group consisting of 211, 7217, 7895, 13308, 14279, 17026, 18271, 20417, 21843, 22069, 22145, 22519, 22539, 23236, 23256, 23402, 23499, 23620, 23871, 24136, 25427, 25866, 26541, 26576, 26689, 26720, 27113, 27164, 27186, 28341, 29160, 29844, 30665,

30830, 31061, 31523, 32326, 32346, 32358, 34909, 34975, 35066, 35096, 35375, 36304, 36712, 36770, 37342, 37412, 37884, 38077, 38300, 38301, 41189, 44408, 44493, 44571, 44670, 45219, 45258, 47261, 48473, 48771, 55292, 56479, 56747, 60620, 60688, 61058, 61129, 61577, 61961, 63351, 63926, 65798, 66043, 66044, 66246, 66318, 66547, 71238, 71283, 71492, 72274, 73762, 74209, 75284, 77347, 77589, 78096, 78606, 78862, 79135, 79146, 79456, 79609, 80086, 80119, 80766, 81110, 81269, 81668, 82433, 82559, 83298, 83821, 84121, 84147, 84543, 84554, 84691, 84727, 85678, 86699, 86700, 86792, 86832, 87045, 87140, 87365, 88342, 88498, 88589, 95502, 96968, 97448, 97568 and 98724.

8. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 2 selected from the group consisting of 23236, 32358, 47261, 48771, 55292, 60688, 72274, 74209, 77589, 79135, 79456, 79609, 80119, 80766, 81110, 82433, 84121, 84147, 85678, 86699, 86832, 87140 and 88589.

9. The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 170719500 to 170766500 of chromosome 6 in human genomic DNA.

10. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 3 selected from the group consisting of 229, 6310, 11840, 11870, 12064, 13392, 16354, 16559, 16935, 17616, 17737, 18321, 18453, 18811, 20020, 21662, 23197, 23446, 24339, 25504, 27174, 28008, 29294, 29759, 30832, 44512, 44850, 45884, 46345, 48589, 53371, 53911, 53990, 55152, 55667, 58952, 59315, 60029, 61477, 62988, 63090, 64021, 65685, 70220, 70323, 70959, 73436, 82945, 82958, 82961, 82964, 82965, 83006, 83025, 83034, 83074, 83132, 83155, 83172, 83174, 83206, 83216, 83234, 83252, 83260, 83263, 83296, 83319, 83322, 83324, 83357, 83375, 83381, 83389, 83443, 83499, 83545, 83566, 83591, 83619, 83698, 83780, 83784, 83826, 83832, 83852, 86297, 86315, 86420, 86460, 86714, 86718, 86736, 86753, 86766, 88162, 88218, 88246, 88255, 88309, 88310, 88471, 88619, 88904, 89044, 90531, 90534, 90613 and 46252.

11. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 3 selected from the group consisting of 229, 6310, 16559, 18453, 25504, 27174, 30832, 44850, 45884, 48589, 61477, 82961 and 46252.

12. The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 27963000 to 27983000 of chromosome 8 in human genomic DNA.

13. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 4 selected from the group consisting of 211, 473, 1536, 5639, 17186, 17335, 25029, 25111, 28811, 28863, 30809, 40985, 45147, 45282, 46168, 46328, 49077, 51925, 52141,

52168, 60852, 62468, 65572, 79089, 79541, 79790, 90843, 90978, 91052, 91131, 91132, 94439 and 94621.

14. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 4 selected from the group consisting of 40985, 46168, 51925 and 52168.

15. The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 44962000 to 45013000 of chromosome 13 in human genomic DNA.

16. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 5 selected from the group consisting of 243, 10208, 15049, 15111, 15272, 15287, 15326, 15327, 17038, 19391, 21702, 22431, 22881, 27744, 32564, 32698, 33104, 33181, 33256, 33543, 35567, 40085, 40482, 45641, 46059, 48504, 48919, 49693, 49874, 50020, 50616, 50719, 55511, 65533, 70529, 75591, 77266, 80368, 82475, 92462, 92480, 95819 and 96275.

17. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 5 selected from the group consisting of 15111, 45641, 46059, 49693, 49874, 50020, 50719, 70529, 82475, 92462, 92480 and 96275.

18. The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 76196500 to 76221500 of chromosome 14 in human genomic DNA.

19. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 6 selected from the group consisting of 218, 1440, 1442, 2611, 4317, 4724, 4788, 5202, 5780, 5974, 6644, 7430, 7938, 8095, 8183, 8312, 8352, 9348, 9378, 9617, 9727, 9834, 9899, 10211, 10377, 10695, 10729, 10730, 11433, 11951, 12697, 12982, 14419, 14501, 14983, 15280, 15475, 15888, 15976, 16307, 16442, 17255, 18948, 19435, 19753, 20021, 20022, 20503, 20590, 21804, 21919, 21990, 22412, 22536, 23432, 23468, 23772, 24325, 24773, 26274, 27440, 28561, 30071, 31764, 33008, 35310, 35460, 37112, 37285, 37747, 38057, 38859, 38860, 39525, 40216, 40281, 41453, 42091, 42513, 42935, 42985, 43003, 43281, 43716, 43866, 44234, 44596, 44871, 45005, 45282, 47178, 47816, 47887, 48134, 48135, 48276, 48400, 48798, 48803, 49146, 49969, 51059, 51064, 53285, 54560, 54748, 54785, 55102, 55644, 55705, 55841, 56623, 56825, 56827, 56892, 59150, 59958, 60231, 60524, 61871, 62226, 63230, 63468, 63787, 65732, 65989, 68832, 69904, 70365, 70886, 73088, 73103, 75934, 75966, 76273, 77943, 78466, 78861, 78872, 79836, 80908, 81509, 83576, 83662, 83782, 84282, 84444, 85129, 85151, 85296, 85809, 86387, 86494, 89786, 89894, 90122, 92067, 92187, 92312, 92824, 93733, 96553 and 96941.

20. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 6 selected from the group consisting of 4788, 8312, 9378, 9727, 9899, 10211, 27440, 40216, 40281, 42091, 43866, 48803, 51059, 55644, 56623, 73103, 78872, 79836, 85129, 92824 and 96941.

21. The method of claim 1, wherein the one or more polymorphic variations are detected within a region spanning chromosome positions 38830000 to 38844000 of chromosome 21 in human genomic DNA.

22. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 7 selected from the group consisting of 231, 882, 960, 1194, 1530, 1673, 2096, 2285, 5873, 7256, 7988, 8222, 8381, 8814, 8915, 9642, 9902, 10619, 10927, 11032, 14377, 15608, 15928, 16296, 17598, 19272, 20084, 20577, 28051, 29466, 29530, 29987, 30012, 30322, 32216, 32516, 32544, 32746, 33137, 33538, 33798, 33802, 33964, 34132, 34210, 34317, 34499, 34753, 34845, 35335, 36423, 36450, 36481, 38447, 38784, 39387, 39458, 39822, 40305, 40869, 40926, 41010, 41134, 41984, 42172, 42753, 43011, 43176, 43320, 43381, 44142, 44383, 44726, 45087, 45141, 45359, 45421, 45456, 45467, 45486, 45709, 45716, 47626, 49413, 49796, 49962, 50075, 50093, 50571, 50615, 50780, 50851, 51459, 53193, 53702, 53736, 53795, 54109, 54126, 54230, 54894, 55455, 55499, 56522, 56662, 56954, 57267, 58282, 58916, 59544, 59666, 59913, 66846, 67245, 67652, 67955, 67966, 68420, 70226, 70810, 72246, 73330, 73457, 74389, 74638, 74640, 75358, 75952, 76098, 77836, 78449, 78507, 80031, 81695, 82775, 82795, 84611, 84657, 84693, 85020, 85048, 85100, 85325, 85452, 85868, 85936, 85990, 86139, 86497, 87236, 87248, 87533, 87912, 88108, 88494, 89598, 90235, 91287, 91359, 92384, 92410, 92900, 94495, 94512, 97777 and 98333.

23. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in SEQ ID NO: 7 selected from the group consisting of 1673, 20577, 33137, 39822, 45716, 49962, 51459, 54894, 55455, 55499, 58282, 68420 and 80031.

24. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in Table A.

25. The method of claim 1, wherein the one or more polymorphic variations are detected at one or more positions in linkage disequilibrium with one or more positions in claim 4, 7, 10, 13, 16, 19, 22 or 24.

26. The method of claim 1, wherein detecting the presence or absence of the one or more polymorphic variations comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to a nucleotide sequence in the nucleic acid and hybridizes to a region adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of a polymorphic variation in the extension products.

27. The method of claim 1, wherein the subject is a human.

28. The method of claim 27, wherein the subject is a human female.

29. The method of claim 27, wherein the subject is a human male.

30. A method for identifying a polymorphic variation associated with osteoarthritis proximal to an incident polymorphic variation associated with osteoarthritis, which comprises:

identifying a polymorphic variation proximal to the incident polymorphic variation associated with osteoarthritis, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising a polymorphic variation;

determining the presence or absence of an association of the proximal polymorphic variant with osteoarthritis.

31. The method of claim 30, wherein the incident polymorphic variation is at one or more positions in claim 4, 7, 10, 13, 16, 19 or 24.

32. The method of claim 30, wherein the proximal polymorphic variation is within a region between about 5 kb 5' of the incident polymorphic variation and about 5 kb 3' of the incident polymorphic variation.

33. The method of claim 30, which further comprises determining whether the proximal polymorphic variation is in linkage disequilibrium with the incident polymorphic variation.

34. The method of claim 30, which further comprises identifying a second polymorphic variation proximal to the identified proximal polymorphic variation associated with osteoarthritis and determining if the second proximal polymorphic variation is associated with osteoarthritis.

35. The method of claim 34, wherein the second proximal polymorphic variant is within a region between about 5 kb 5' of the incident polymorphic variation and about 5 kb 3' of the proximal polymorphic variation associated with osteoarthritis.

36. An isolated nucleic acid comprising a nucleotide sequence selected from the group consisting of:

- (a) a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;
- (b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;
- (c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;
- (d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising a polymorphic variation; and

- (e) a nucleotide sequence complementary to the nucleotide sequences of (a), (b), (c), or (d);

wherein the nucleotide sequence comprises a polymorphic variation associated with osteoarthritis selected from the group consisting of in SEQ ID NO: 1 a guanine at position 13150, a thymine at position 21046, an adenine at position 23170, an adenine at position 25028, a guanine at position 44580, a guanine at position 62906, a cytosine at position 64664 and a cytosine at position 83517; in SEQ ID NO: 2 an adenine at position 23236, a cytosine at position 32358, a guanine at position 47261, a guanine at position 48771, a cytosine at position 55292, an adenine at position 60688, a guanine at position 72274, a guanine at position 74209, a cytosine at position 77589, an adenine at position 79135, a thymine at position 79456, an adenine at position 79609, an adenine at position 80119, a cytosine at position 80766, an adenine at position 81110, a cytosine at position 82433, a cytosine at position 84121, a thymine at position 84147, a cytosine at position 85678, a thymine at position 86699, an adenine at position 86832, a guanine at position 87140 and an adenine at position 88589; in SEQ ID NO: 3 a thymine at position 229, a guanine at position 6310, a thymine at position 16559, an adenine at position 18453, an adenine at position 25504, an adenine at position 27174, an adenine at position 30832, a guanine at position 44850, an adenine at position 45884, an adenine at position 48589, a cytosine at position 61477, a cytosine at position 82961 and a thymine at position 46252; in SEQ ID NO: 4 a cytosine at position 40985, a guanine at position 46168, a thymine at position 51925 and a cytosine at position 52168; in SEQ ID NO: 5 a guanine at position 15111, a thymine at position 45641, an adenine at position 46059, a cytosine at position 49693, an adenine at position 49874, an adenine at position 50020, a guanine at position 50719, an adenine at position 70529, an adenine at position 82475, a thymine at position 92462, a thymine at position 92480 and a cytosine at position 96275; in SEQ ID NO: 6 a guanine at position 4788, a thymine at position 8312, a deletion at position 9378, a cytosine at position 9727, a guanine at position 9899, a

cytosine at position 10211, a guanine at position 27440, a guanine at position 40216, a cytosine at position 40281, an adenine at position 42091, a guanine at position 43866, an adenine at position 48803, an adenine at position 51059, an adenine at position 55644, a cytosine at position 56623, a cytosine at position 73103, an adenine at position 78872, a guanine at position 79836, a cytosine at position 85129, a guanine at position 92824 and an adenine at position 96941; in SEQ ID NO: 7 a guanine at position 1673, a thymine at position 20577, a guanine at position 33137, a guanine at position 39822, an adenine at position 45716, a guanine at position 49962, an adenine at position 51459, a cytosine at position 54894, an adenine at position 55455, an adenine at position 55499, a guanine at position 58282, an adenine at position 68420 and a thymine at position 80031; and an allele associated with osteoporosis in Table A for positions rs552, rs12904, rs2282146, rs734784, rs1042164, rs749670, rs955592, rs1143016, rs755248, rs1055055, rs835409, rs927663, rs8162, rs831038, rs33079, rs1710880, rs1078153, rs799570, rs1282730, rs1518875, rs1568694, rs905042, rs1957723, rs794018, rs707723, rs893861, rs1914903, rs2062232, rs26609, rs1370987, rs1012414, rs435903, rs1248, rs703508, rs226465, rs241448, rs763155, rs1040461, rs462832, rs804194, rs1022646, rs756519, rs1042327, rs8770, rs1569112, rs1563055, rs805623, rs1019850, rs1599931, AA, rs912428, rs279941, rs1062230, rs1859911, rs1477261, rs1191119, rs657780, rs1393890, rs1478714, rs868213, rs690115, rs1465501, rs899173, rs10477, rs926393, rs465271, rs1888475, rs13847 and rs738658.

37. An oligonucleotide comprising a nucleotide sequence complementary to a portion of the nucleotide sequence of (a), (b), (c), or (d) in claim 36, wherein the 3' end of the oligonucleotide is adjacent to a polymorphic variation associated with osteoarthritis.

38. A microarray comprising an isolated nucleic acid of claim 36 linked to a solid support.

39. An isolated polypeptide encoded by the isolated nucleic acid sequence of claim 36.

40. A method for identifying a candidate therapeutic for treating osteoarthritis, which comprises:

(a) introducing a test molecule to a system which comprises a nucleic acid comprising a nucleotide sequence selected from the group consisting of:

- (i) a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;
- (ii) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;
- (iii) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(iv) a fragment of a nucleotide sequence of (a), (b), or (c); or
introducing a test molecule to a system which comprises a protein encoded by a nucleotide sequence of (i), (ii), (iii), or (iv); and

(b) determining the presence or absence of an interaction between the test molecule and the nucleic acid or protein,

whereby the presence of an interaction between the test molecule and the nucleic acid or protein identifies the test molecule as a candidate therapeutic for treating osteoarthritis.

41. The method of claim 40, wherein the system is an animal.

42. The method of claim 40, wherein the system is a cell.

43. The method of claim 40, wherein the nucleotide sequence comprises one or more polymorphic variations associated with osteoarthritis.

44. The method of claim 43, wherein the one or more polymorphic variations associated with osteoarthritis are at one or more positions in claim 4, 7, 10, 13, 16, 19 or 24.

45. A method for treating osteoarthritis in a subject, which comprises contacting one or more cells of a subject in need thereof with a nucleic acid, wherein the nucleic acid comprises a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(d) a fragment of a nucleotide sequence of (a), (b), or (c); and

(e) a nucleotide sequence complementary to the nucleotide sequences of (a), (b), (c), or (d);

whereby contacting the one or more cells of the subject with the nucleic acid treats the osteoarthritis in the subject.

46. The method of claim 45, wherein the nucleic acid is RNA or PNA.

47. The method of claim 46, wherein the nucleic acid is duplex RNA.

48. A method for treating osteoarthritis in a subject, which comprises contacting one or more cells of a subject in need thereof with a protein, wherein the protein is encoded by a nucleotide sequence which comprises a polynucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(d) a fragment of a nucleotide sequence of (a), (b), or (c);

whereby contacting the one or more cells of the subject with the protein treats the osteoarthritis in the subject.

49. A method for treating osteoarthritis in a subject, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with osteoarthritis in a nucleic acid sample from a subject, wherein the one or more polymorphic variation are detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising a polymorphic variation; and

administering an osteoarthritis treatment to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

50. The method of claim 49, wherein the one or more polymorphic variations are detected at one or more positions in claim 4, 7, 10, 13, 16, 19 or 24.

51. The method of claim 49, wherein the treatment is selected from the group consisting of administering a corticosteroid, a nonsteroidal anti-inflammatory drug (NSAID), a cyclooxygenase-2 (COX-2) inhibitor, an antibody, a glucocorticoid, hyaluronic acid, chondroitin sulfate, glucosamine or acetaminophen; prescribing a heat/cold regimen or a joint protection regimen; performing joint surgery; prescribing a weight control regimen; and combinations of the foregoing.

52. A method for detecting or preventing osteoarthritis in a subject, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with osteoarthritis in a nucleic acid sample from a subject, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising a polymorphic variation; and

administering an osteoarthritis prevention or detection procedure to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

53. The method of claim 52, wherein the one or more polymorphic variations are detected at one or more positions in claim 4, 7, 10, 13, 16, 19 or 24.

54. The method of claim 52, wherein the osteoarthritis prevention is selected from the group consisting of administering a corticosteroid, a nonsteroidal anti-inflammatory drug (NSAID), a cyclooxygenase-2 (COX-2) inhibitor, an antibody, a glucocorticoid, hyaluronic acid, chondrotin sulfate, glucosamine or acetaminophen; prescribing a heat/cold regimen or a joint protection regimen; performing joint surgery; prescribing a weight control regimen; and combinations of the foregoing.

55. A method of targeting information for preventing or treating osteoarthritis to a subject in need thereof, which comprises:

detecting the presence or absence of one or more polymorphic variations associated with osteoarthritis in a nucleic acid sample from a subject, wherein the polymorphic variation is detected in a nucleotide sequence selected from the group consisting of:

(a) a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(b) a nucleotide sequence which encodes a polypeptide encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(c) a nucleotide sequence which encodes a polypeptide that is 90% or more identical to the amino acid sequence encoded by a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A;

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising a polymorphic variation; and

directing information for preventing or treating osteoarthritis to a subject in need thereof based upon the presence or absence of the one or more polymorphic variations in the nucleic acid sample.

56. The method of claim 55, wherein the one or more polymorphic variations are detected at one or more positions in claim 4, 7, 10, 13, 16, 19 or 24.

57. A composition comprising a cell from a subject having osteoarthritis or at risk of osteoarthritis and an antibody that specifically binds to a protein, polypeptide or peptide encoded by a nucleotide sequence identical to or 90% or more identical to a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A.

58. The composition of claim 57, wherein the antibody specifically binds to an epitope comprising an amino acid encoded by rs734784, rs1042164, rs749670, rs955592, rs241448 and rs1040461.

59. A composition comprising a cell from a subject having osteoarthritis or at risk of osteoarthritis and a RNA, DNA, PNA or ribozyme molecule comprising a nucleotide sequence identical to or 90% or more identical to a portion of a nucleotide sequence in SEQ ID NO: 1-7 or referenced in Table A.

60. The composition of claim 59, wherein the RNA molecule is a short inhibitory RNA molecule.